FIG. 1

FIG. 1A

```
   1 tcttcctacccatctgctccccagagggctgcctgctgtgcacttgggtcctggagcccttctccacccggatagattcctcacccttggcccgcctttg

 101 ccccaccctactctgcccagaagtgcaagagcctaagccgcctccatggccccaggaaggattcaggggagaggccccaaacagggagccacgccagcca

                          -20                -10
                 MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
 201 gacaccccggccagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTG

       10                  20                   30                  40
    LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
 301 ACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT

                50                  60                  70
    ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
 401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG

             80                  90                  100
    MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
 501 ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCC

       110                 120                 130                 140
    GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
 601 TTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT

                150                 160                 170
    LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
 701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCCTCACACTGAACGAGCTC

             180                 190                 200
    Pro[AsnArgThr]SerGlyLeuLeuGluThr[AsnPheThr]AlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
 801 CCAAACAGGACTTCTGGATTGTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGA

       210                 220                 230                 240
    ProGlyLeuLeu[AsnGlnThr]SerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeu[AsnGlyThr]ArgGlyLeuPhePro
 901 TTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTGGACCAAATCCCCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTCC

                250                 260                 270
    GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001 TGGACCCTCACGCAGGACCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCCTTCC

             280                 290                 300
    ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisProLeuLeuProAspProSerAla
1101 CCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCACCCCTGTGGTCCAGCTCCACCCCCTGCTTCCTGACCCTTCTG

       310                 320                 330
    ProThrProThrProThrSerProLeuLeu[AsnThrSer]TyrThrHisSerGln[AsnLeuSer]GlnGluGly
1201 CTCCAACGCCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCCAGAATCTGTCTCAGGAAGGGTAAggttctcagacactgccgacatc

1301 agcattgtctcatgtacagctcccttccctgcagggcgcccctgggagacaactggacaagatttcctactttctcctgaaacccaaagccctggtaaaa

1401 gggatacacaggactgaaaagggaatcatttttcactgtacattataaaccttcagaagctatttttttaagctatcagcaatactcatcagagcagcta

1501 gctctttggtctattttctgcagaaatttgcaactcactgattctctacatgctctttttctgtgataactctgcaaaggcctgggctggcctggcagtt

1601 gaacagagggagagactaaccttgagtcagaaaacagagaaagggtaatttcctttgcttcaaattcaaggcctfccaacgcccccatcccctttactat

1701 cattctcagtgggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaaaaaaaaaaaaaaa
```

FIG. 1B

FIG. 1A

```
  1 tcttcctacccatctgctccccagagggctgcctgctgtgcacttgggtcctggagcccttctccacccggatagattcctcacccttggcccgcctttg

101 ccccaccctactctgcccagaagtgcaagagcctaagccgcctccatggccccaggaaggattcaggggagaggccccaaacagggagccacgccagcca

                         -20                         -10
                    MetGluLeuThrGluLeuLeuLeuValValMetLeuLeuLeuThrAlaArgLeuThrLeuSerSerProAlaProProAlaCysAsp
201 gacaccccggccagaATGGAGCTGACTGAATTGCTCCTCGTGGTCATGCTTCTCCTAACTGCAAGGCTAACGCTGTCCAGCCCGGCTCCTCCTGCTTGTG

     10                          20                          30                                   40
   LeuArgValLeuSerLysLeuLeuArgAspSerHisValLeuHisSerArgLeuSerGlnCysProGluValHisProLeuProThrProValLeuLeu
301 ACCTCCGAGTCCTCAGTAAACTGCTTCGTGACTCCCATGTCCTTCACAGCAGACTGAGCCAGTGCCCAGAGGTTCACCCTTTGCCTACACCTGTCCTGCT

                         50                          60                          70
  ProAlaValAspPheSerLeuGlyGluTrpLysThrGlnMetGluGluThrLysAlaGlnAspIleLeuGlyAlaValThrLeuLeuLeuGluGlyVal
401 GCCTGCTGTGGACTTTAGCTTGGGAGAATGGAAAACCCAGATGGAGGAGACCAAGGCACAGGACATTCTGGGAGCAGTGACCCTTCTGCTGGAGGGAGTG

              80                          90                          100
MetAlaAlaArgGlyGlnLeuGlyProThrCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeuLeuGlyAlaLeuGlnSerLeuLeu
501 ATGGCAGCACGGGGACAACTGGGACCCACTTGCCTCTCATCCCTCCTGGGGCAGCTTTCTGGACAGGTCCGTCTCCTCCTTGGGGCCCTGCAGAGCCTCC

      110                         120                         130                                  140
   GlyThrGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProAsnAlaIlePheLeuSerPheGlnHisLeuLeuArgGlyLysValArgPhe
601 TTGGAACCCAGCTTCCTCCACAGGGCAGGACCACAGCTCACAAGGATCCCAATGCCATCTTCCTGAGCTTCCAACACCTGCTCCGAGGAAAGGTGCGTTT

                         150                         160                         170
  LeuMetLeuValGlyGlySerThrLeuCysValArgArgAlaProProThrThrAlaValProSerArgThrSerLeuValLeuThrLeuAsnGluLeu
701 CCTGATGCTTGTAGGAGGGTCCACCCTCTGCGTCAGGCGGGCCCCACCCACCACAGCTGTCCCCAGCAGAACCTCTCTAGTCCTCACACTGAACGAGCTC

               180                         190                         200
  ProAsnArgThrSerGlyLeuLeuGluThrAsnPheThrAlaSerAlaArgThrThrGlySerGlyLeuLeuLysTrpGlnGlnGlyPheArgAlaLysIle
801 CCAAACAGGACTTCTGGATTGTTGGAGACAAACTTCACTGCCTCAGCCAGAACTACTGGCTCTGGGCTTCTGAAGTGGCAGCAGGGATTCAGAGCCAAGA
```

FIG. 1B

```
             210                        220                          230                         240
          ProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyTyrLeuAsnArgIleHisGluLeuLeuAsnGlyThrArgGlyLeuPhePro
 901  TTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTGGACCAAATCCCCGGATACCTGAACAGGATACACGAACTCTTGAATGGAACTCGTGGACTCTTTCC

                         250                         260                          270
        GlyProSerArgArgThrLeuGlyAlaProAspIleSerSerGlyThrSerAspThrGlySerLeuProProAsnLeuGlnProGlyTyrSerProSer
1001  TGGACCCTCACGCAGGACCCTAGGAGCCCCGGACATTTCCTCAGGAACATCAGACACAGGCTCCCTGCCACCCAACCTCCAGCCTGGATATTCTCCTTCC

                 280                         290                          300
      ProThrHisProProThrGlyGlnTyrThrLeuPheProLeuProProThrLeuProThrProValValGlnLeuHisPrcLeuLeuProAspProSerAla
1101  CCAACCCATCCTCCTACTGGACAGTATACGCTCTTCCCTCTTCCACCCACCTTGCCCACCCCTGTGGTCCAGCTCCACCCCCTGCTTCCTGACCCTTCTG

          310                         320                        330
        ProThrProThrProThrSerProLeuLeuAsnThrSerTyrThrHisSerGlnAsnLeuSerGlnGluGly
1201  CTCCAACGCCCACCCCTACCAGCCCTCTTCTAAACACATCCTACACCCACTCCCAGAATCTGTCTCAGGAAGGGTAAggttctcagacactgccgacatc

1301  agcattgtctcatgtacagctcccttccctgcagggcgcccctgggagacaactggacaagatttcctactttctcctgaaacccaaagccctggtaaaa

1401  gggatacacaggactgaaaagggaatcatttttcactgtacattataaaccttcagaagctatttttttaagctatcagcaatactcatcagagcagcta

1501  gctctttggtctattttctgcagaaatttgcaactcactgattctctacatgctctttttctgtgataactctgcaaaggcctgggctggcctggcagtt

1601  gaacagagggagagactaaccttgagtcagaaaacagagaaagggtaatttcctttgcttcaaattcaaggccttccaacgcccccatcccctttactat

1701  cattctcagtgggactctgatcccatattcttaacagatctttactcttgagaaatgaataagctttctctcagaaaaaaaaaaaaaaaaaaaa
```

FIG. 2

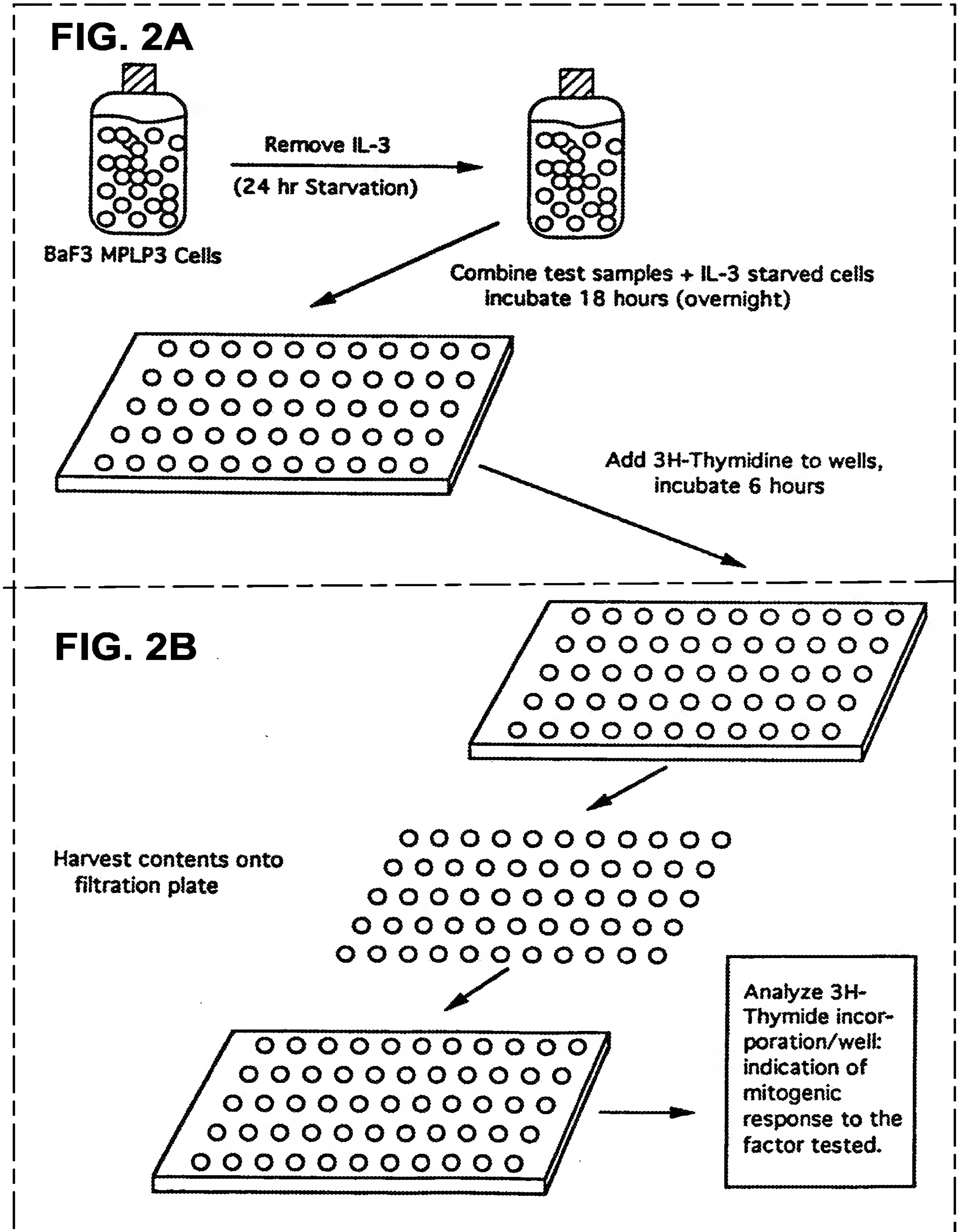


FIG. 2A
Remove IL-3
(24 hr Starvation)
BaF3 MPLP3 Cells
Combine test samples + IL-3 starved cells
incubate 18 hours (overnight)
Add 3H-Thymidine to wells,
incubate 6 hours
FIG. 2B
Harvest contents onto
filtration plate
Analyze 3H-
Thymide incor-
poration/well:
indication of
mitogenic
response to the
factor tested.

FIG. 2A

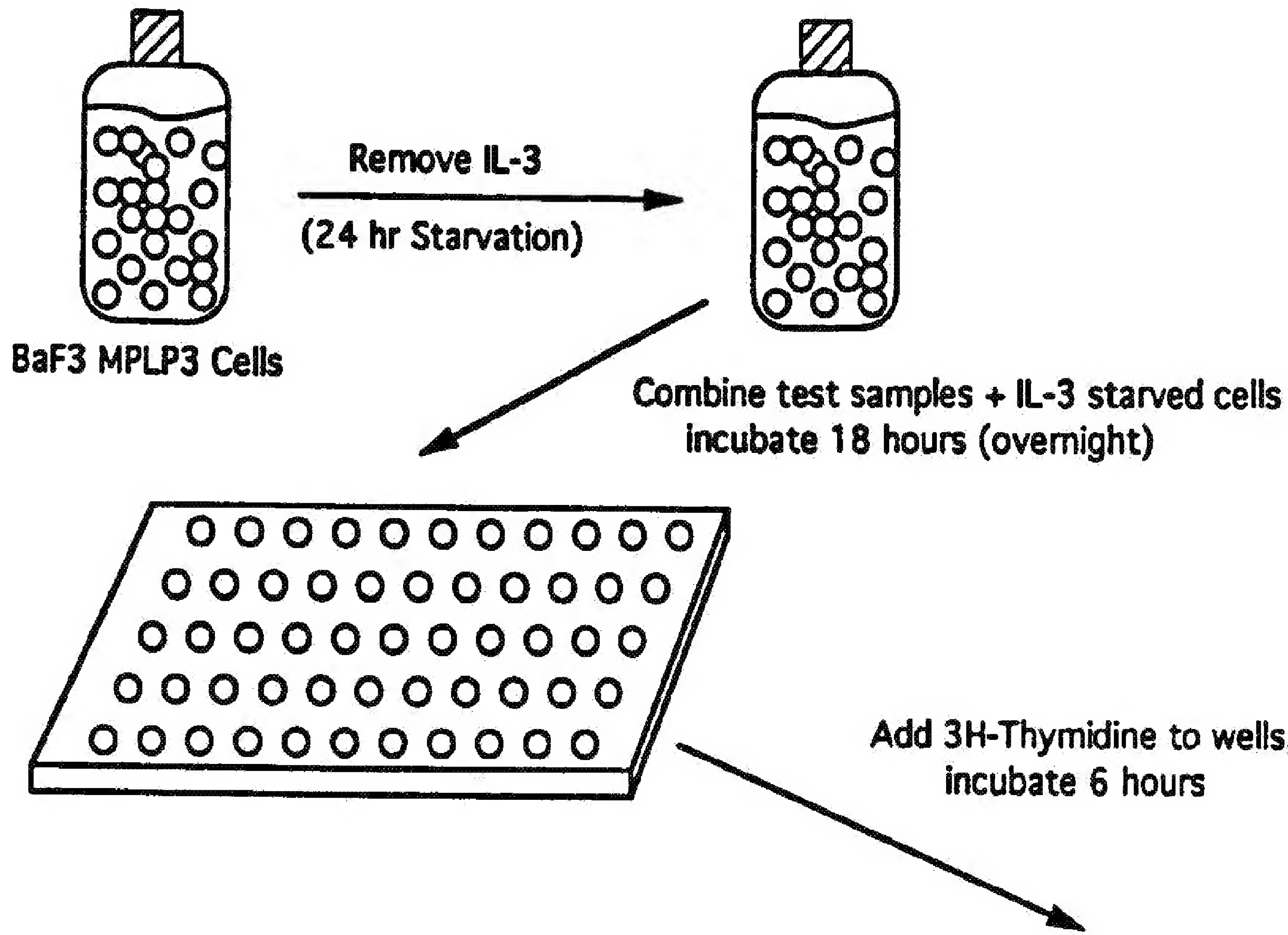
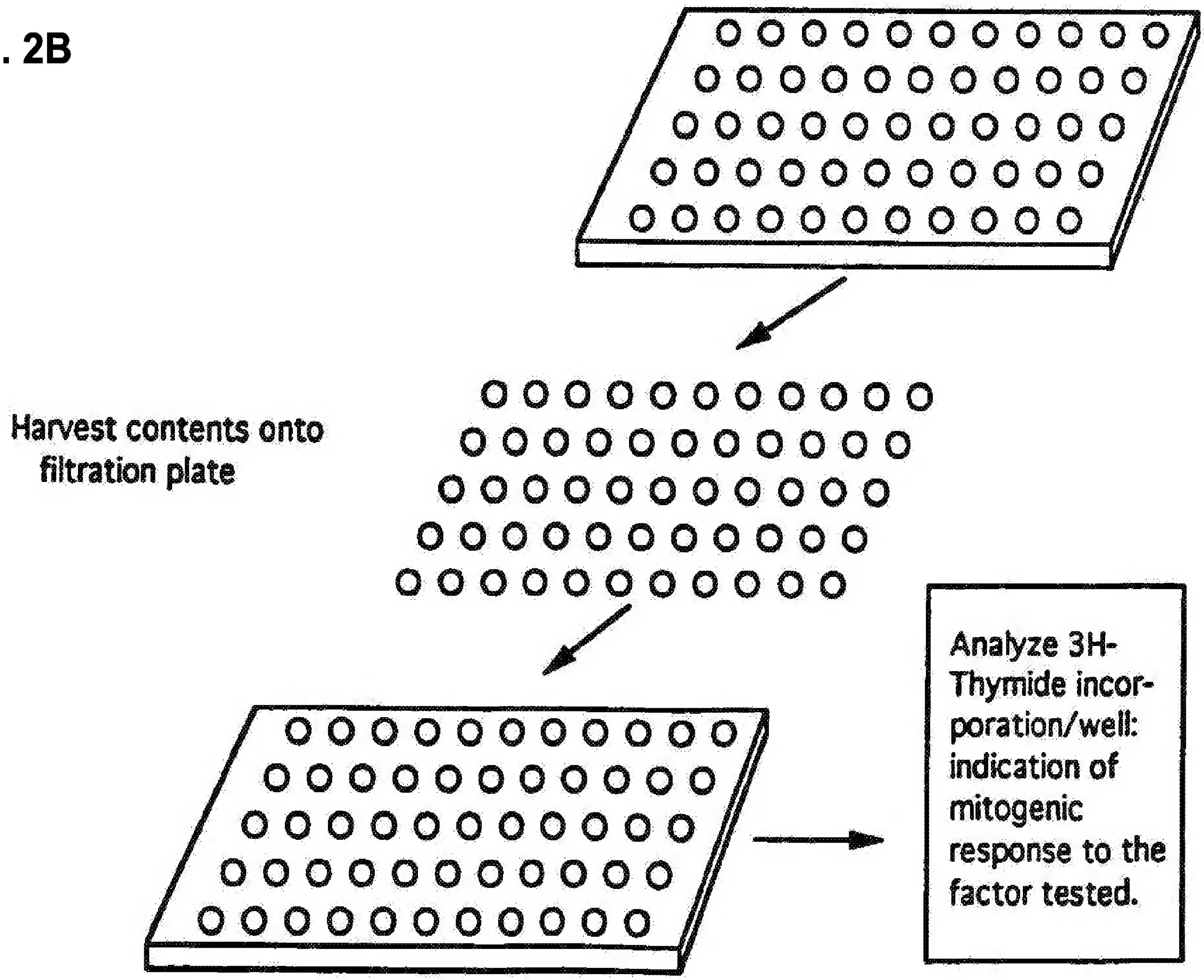

BaF3 MPLP3 Cells
Remove IL-3
(24 hr Starvation)
Combine test samples + IL-3 starved cells
incubate 18 hours (overnight)
Add 3H-Thymidine to wells,
incubate 6 hours

FIG. 2B


Harvest contents onto filtration plate
Analyze 3H-Thymide incorporation/well: indication of mitogenic response to the factor tested.

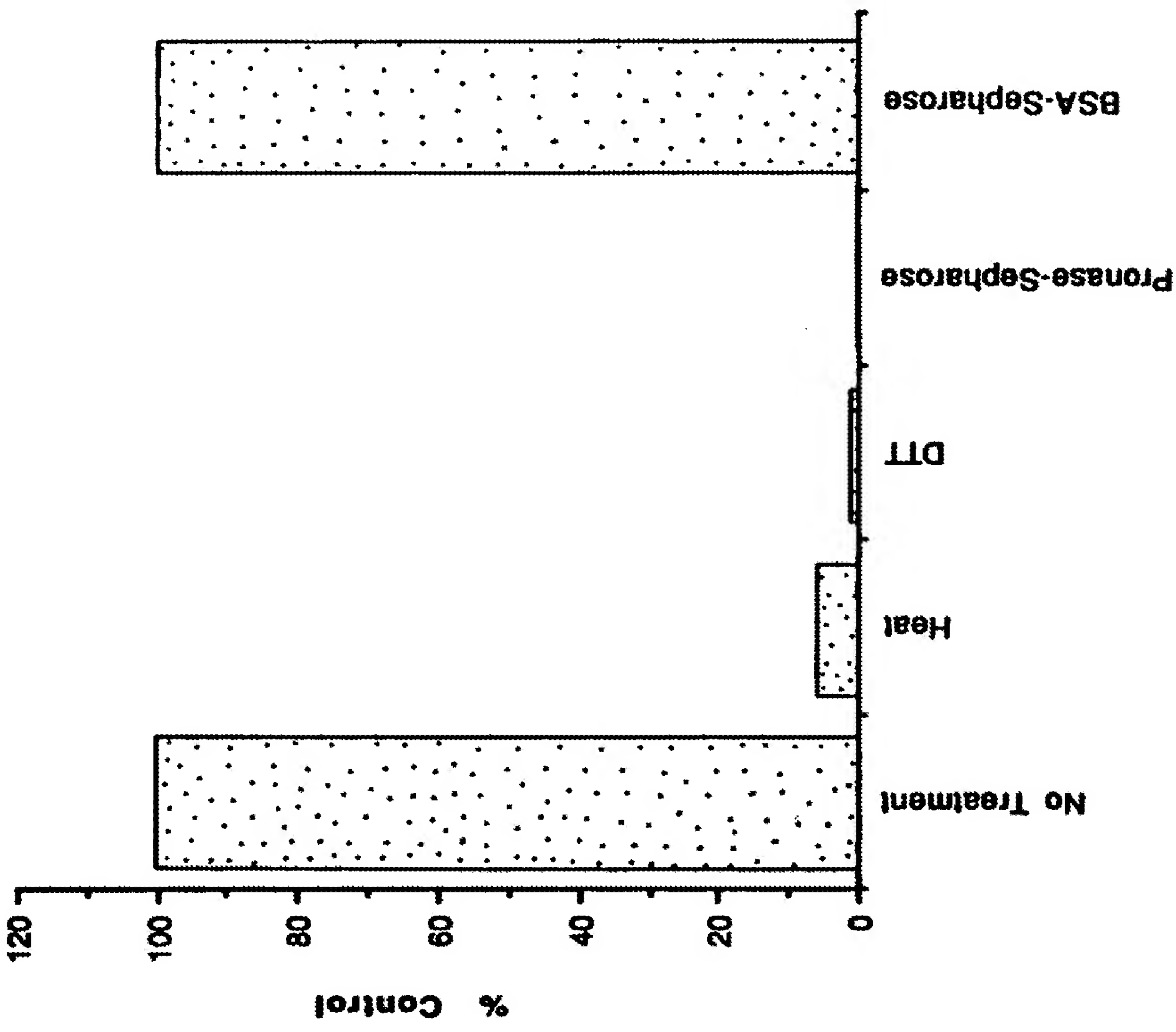

% Control
120
100
80
60
40
20
0
No Treatment
Heat
DTT
Pronase-Sepharose
BSA-Sepharose

FIG. 3

FIG. 4

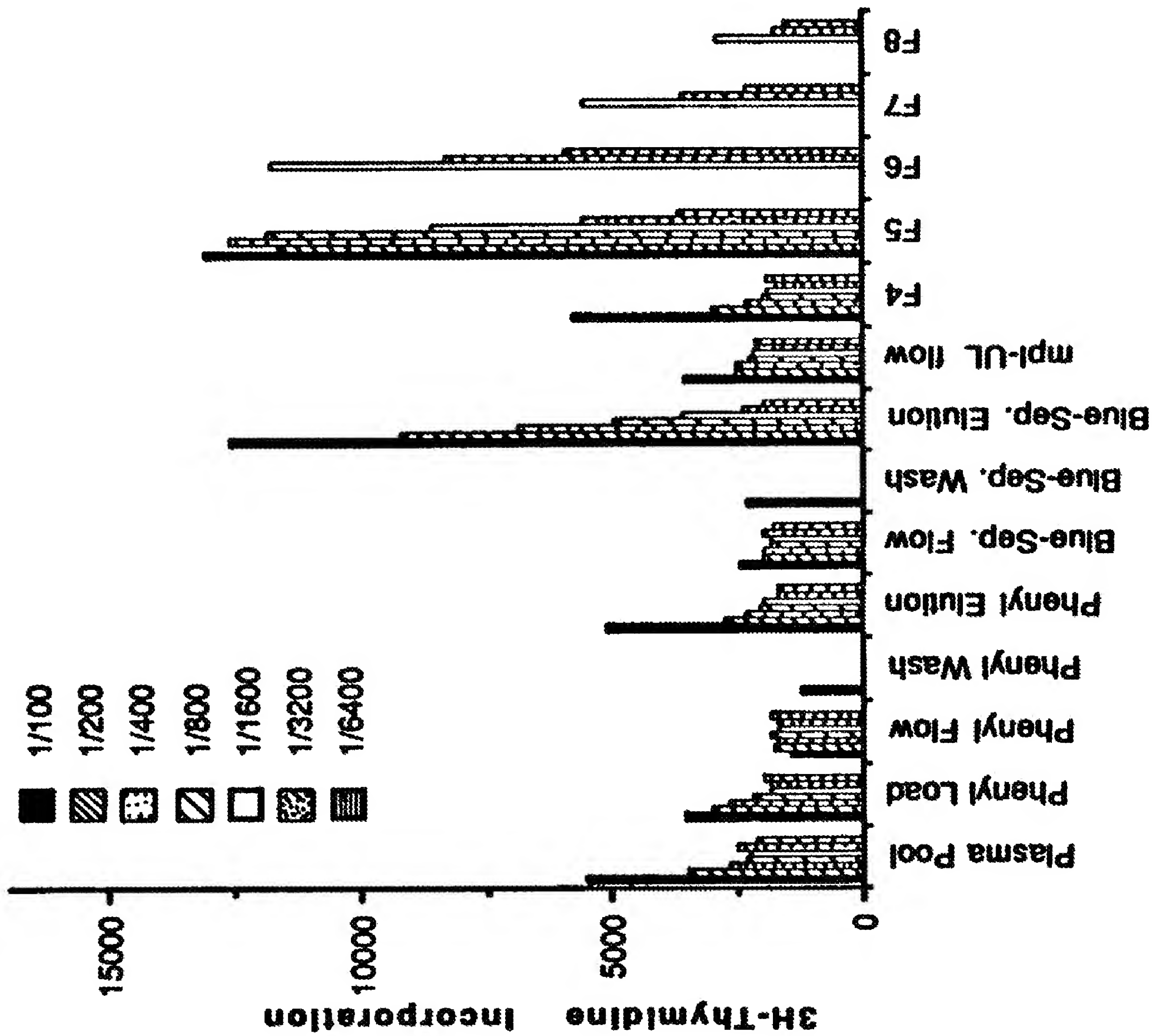

3H-Thymidine Incorporation
0
5000
10000
15000
Plasma Pool
Phenyl Load
Phenyl Flow
Phenyl Wash
Phenyl Elution
Blue-Sep. Flow
Blue-Sep. Wash
Blue-Sep. Elution
mpl-UL flow
F4
F5
F6
F7
F8
1/100
1/200
1/400
1/800
1/1600
1/3200
1/6400

FIG. 5

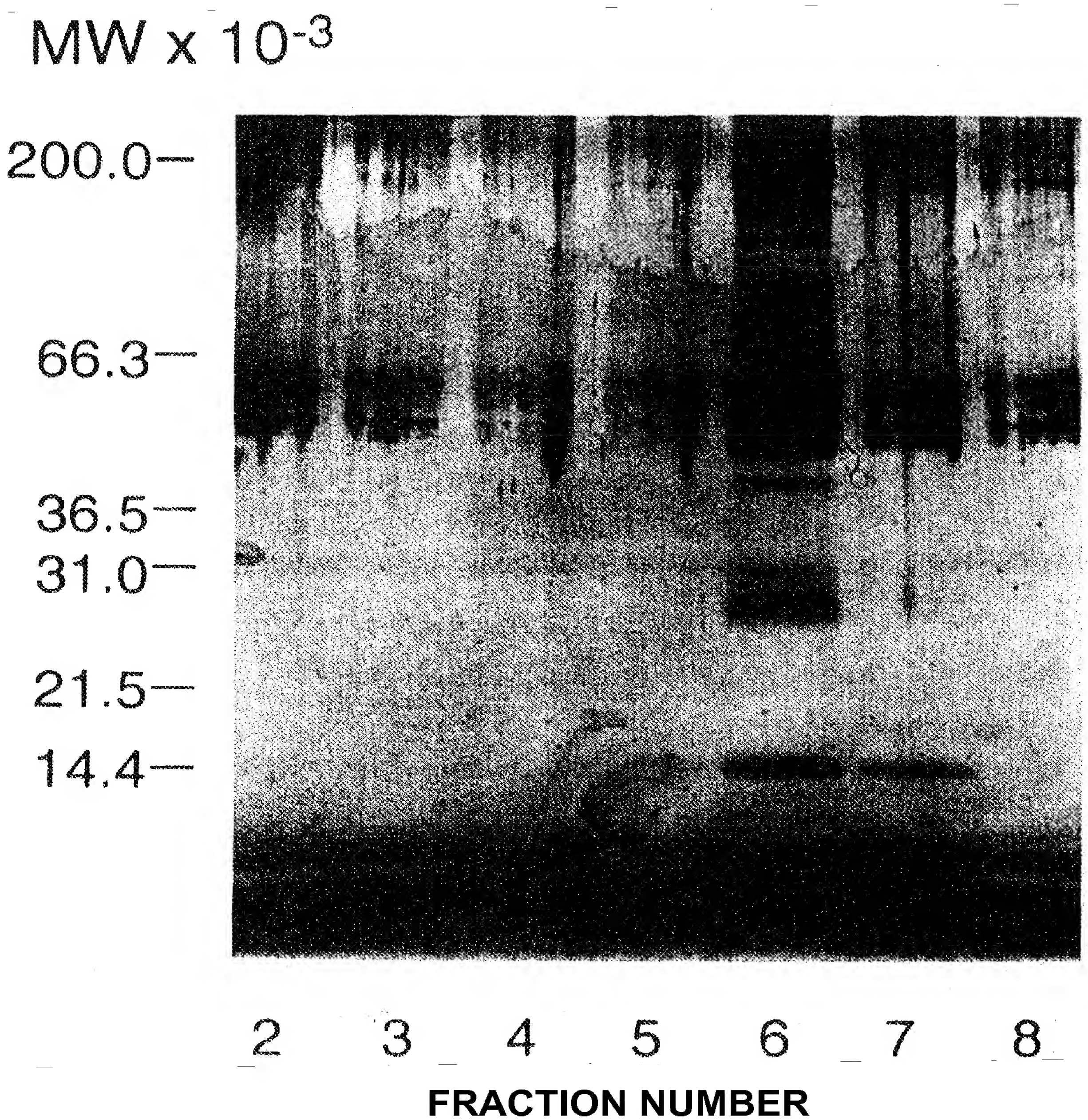


FIG.6

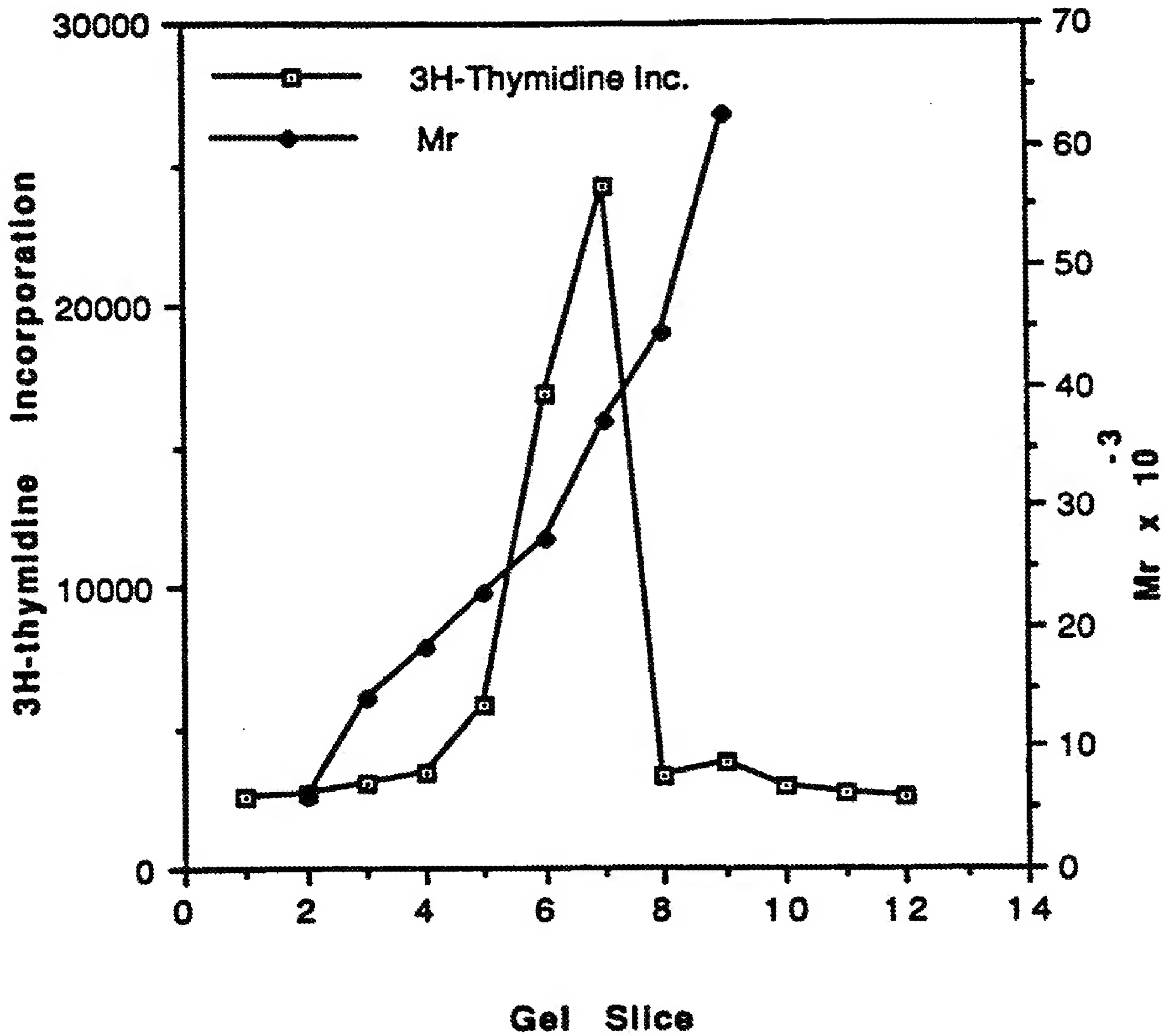
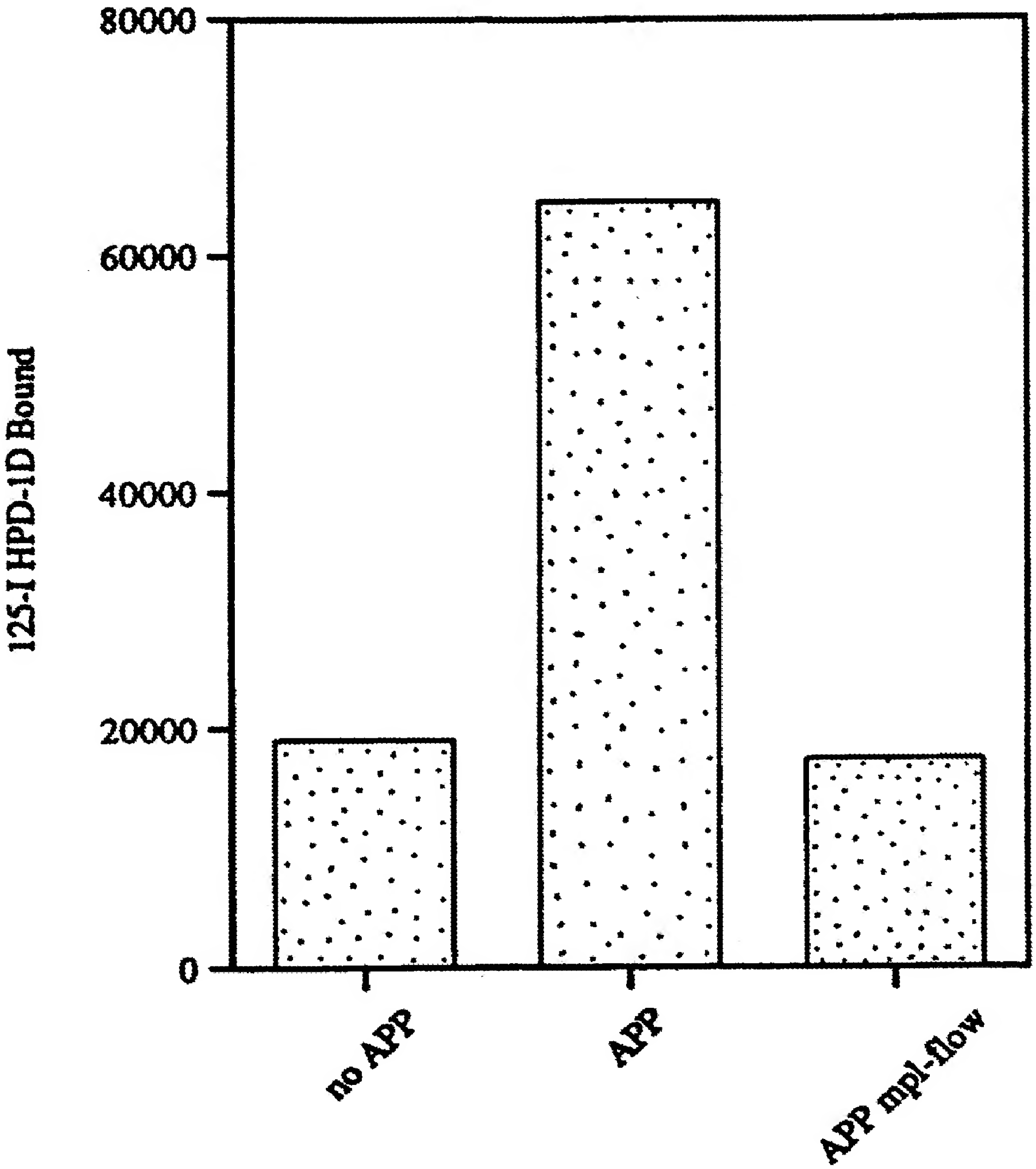

3H-Thymidine Inc.
Mr
3H-thymidine Incorporation
30000
20000
10000
0
70
60
50
40
30
20
10
0
Mr x 10 -3
0
2
4
6
8
10
12
14
Gel Slice

FIG. 7


80000
60000
40000
20000
0
125-I HPD-1D Bound
no APP
APP
APP mpl-flow

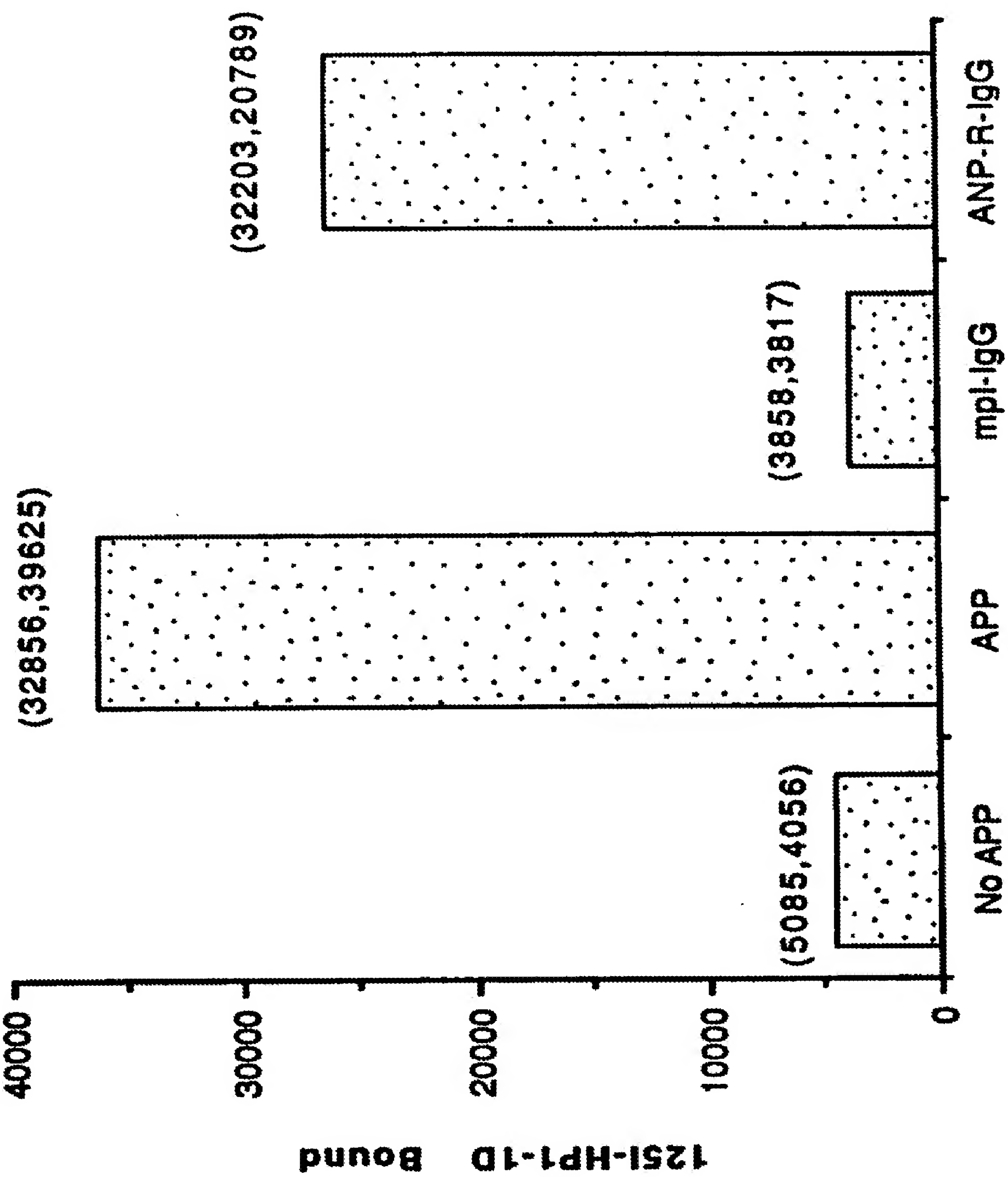

(32203,20789)
(3858,3817)
(32856,39625)
(5085,4056)
No APP
APP
mpl-IgG
ANP-R-IgG
40000
30000
20000
10000
0
125I-HP1-1D Bound

FIG. 8

FIG. 9

```
                                                                                            -10
                                                                            L L L V  V M L  L L T
  1 GAATTCCTGG AATACCAGCT GACAATGATT TCCTCCTCAT CTTTCAACCT CACCTCTCCT CATCTAAGAA TTGCTCCTCG TGGTCATGCT TCTCCTAACT
    CTTAAGGACC TTATGGTCGA CTGTTACTAA AGGAGGAGTA GAAAGTTGGA GTGGAGAGGA GTAGATTCTT AACGAGGAGC ACCAGTACGA AGAGGATTGA

                                                 10                            20
    A R L T  L S S  P A P  P A C D  L R V  L S K  L L R D  S H V  L H S  R L
101 GCAAGGCTAA CGCTGTCCAG CCCGGCTCCT CCTGCTTGTG ACCTCCGAGT CCTCAGTAAA CTGCTTCGTG ACTCCCATGT CCTTCACAGC AGACTGGTGA
    CGTTCCGATT GCGACAGGTC GGGCCGAGGA GGACGAACAC TGGAGGCTCA GGAGTCATTT GACGAAGCAC TGAGGGTACA GGAAGTGTCG TCTGACCACT

201 GAACTCCCAA CATTATCCCC TTTATCCGCG TAACTGGTAA GACACCCATA CTCCCAGGAA GACACCATCA CTTCCTCTAA CTCCTTGACC CAATGACTAT
    CTTGAGGGTT GTAATAGGGG AAATAGGCGC ATTGACCATT CTGTGGGTAT GAGGGTCCTT CTGTGGTAGT GAAGGAGATT GAGGAACTGG GTTACTGATA

301 TCTTCCCATA TTGTCCCCAC CTACTGATCA CACTCTCTGA CAAGAATTAT TCTTCACAAT ACAGCCCGCA TTTAAAAGCT CTCGTCTAGA
    AGAAGGGTAT AACAGGGGTG GATGACTAGT GTGAGAGACT GTTCTTAATA AGAAGTGTTA TGTCGGGCGT AAATTTTCGA GAGCAGATCT
```

FIG. 10

```
h-ML      1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
h-epo     1 APPRLICDSRVLERYLLEAKEAENITTGCAEHCSLNENITVPDTKVNFYA

h-ML     51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLS--SLLGQLSGQVR
h-epo    51 WKRMEVGQQAVEVWQGLALLSEAVLRGQALLVNSSQPWEPLQLHVDKAVS

h-ML     99 LL--LGALQSLLGTQ---LPPQGRTTAHKDPNAIFLSFQHLLRGKVRFL-
h-epo   101 GLRSLTTLLRALGAQKEAISPPDAASAAPLRTITADTFRKLFRVYSNFLR

h-ML    143 --MLVGGSTLCVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASA
h-epo   151 GKLKLYTGEACRTGDR

h-ML    191 RTTGSGLLKWQQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLF

h-ML    241 PGPSRRTLGAPDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPP

h-ML    291 TLPTPVVQLHPLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
```

FIG. 11

FIG.11A

```
hML    1   SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML2   1   SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML3   1   SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML4   1   SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE

hML    51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML2   51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML3   51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML4   51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL

hML    101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML2   101 LGALQSLLGT----QGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML3   101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK-DFW-IVGDKLH
hML4   101 LGALQSLLGT----QGRTTAHKDPNAIFLSFQHLLRGK-DFW-IVGDKLH

hML    151 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML2   147 CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML3   149 CLSQ---------NYWL---------WASEVAAGIQSQDSWSAEPNLQ--
hML4   145 CLSQ---------NYWL---------WASEVAAGIQSQDSWSAEPNLQ--
```

```
hML    201 QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML2   197 QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML3   179 VPGPNPRIP---EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA
hML4   175 VPGPNPRIP---EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA

hML    251 PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML2   247 PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML3   226 TQ-----------PPAWIFSFP-----NPSSYWTVYALPSS---------
hML4   222 TQ-----------PPAWIFSFP-----NPSSYWTVYALPSS---------

hML    301 PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML2   297 PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML3   251 THLAHPCGPAPPPAS-----------------
hML4   247 THLAHPCGPAPPPAS-----------------
```

FIG.11B

FIG. 11A

```
hML     1  SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML2    1  SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML3    1  SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
hML4    1  SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE

hML    51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML2   51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML3   51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
hML4   51  WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL

hML   101  LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML2  101  LGALQSLLGT....QGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
hML3  101  LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGK.DFW.IVGDKLH
hML4  101  LGALQSLLGT....QGRTTAHKDPNAIFLSFQHLLRGK.DFW.IVGDKLH

hML   151  CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML2  147  CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW
hML3  149  CLSQ..........NYWL........WASEVAAGIQSQDSWSAEPNLQ..
hML4  145  CLSQ..........NYWL........WASEVAAGIQSQDSWSAEPNLQ..
```

FIG. 11B

```
hML   201  QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML2  197  QQGFRAKIPGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLGA
hML3  179  VPGPNPRIP...EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA
hML4  175  VPGPNPRIP...EQDTRTLEWNSWTLSWTLTQDPRSPGHFLRNIRHRLPA

hML   251  PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML2  247  PDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPTPVVQLH
hML3  226  TQ...........PPAWIFSFP.....NPSSYWTVYALPSS.........
hML4  222  TQ...........PPAWIFSFP.....NPSSYWTVYALPSS.........

hML   301  PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML2  297  PLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
hML3  251  THLAHPCGPAPPPAS.................
hML4  247  THLAHPCGPAPPPAS.................
```

FIG. 12A

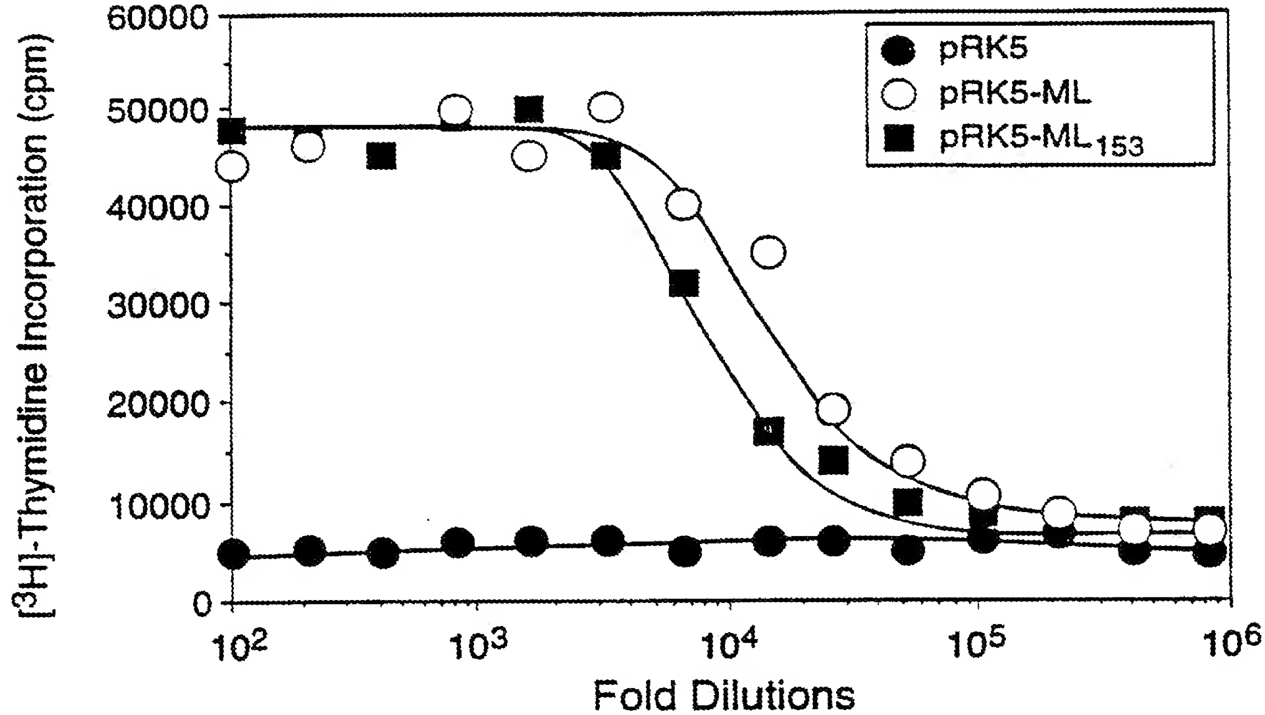


FIG. 12B

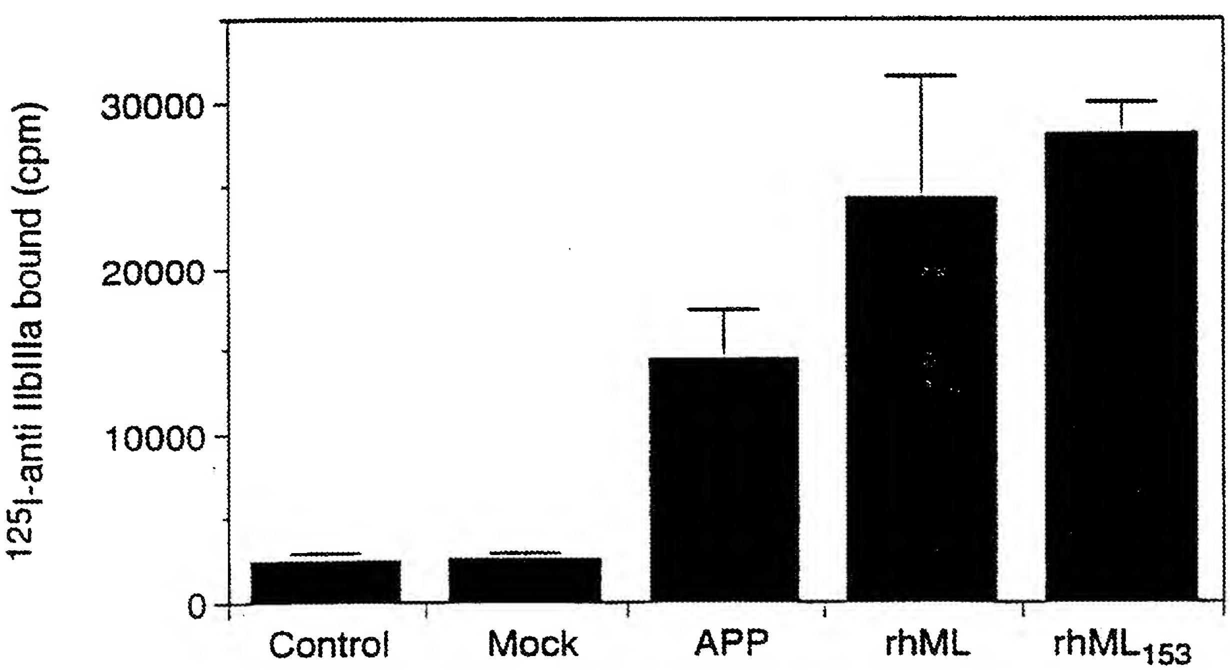


FIG. 12C

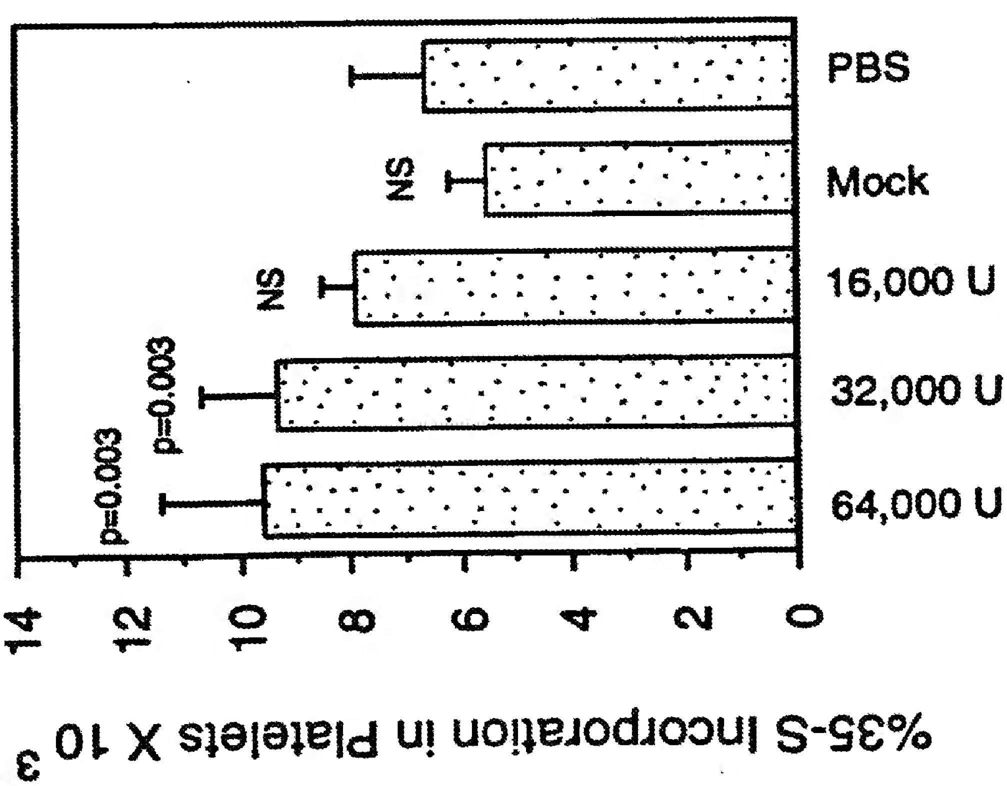
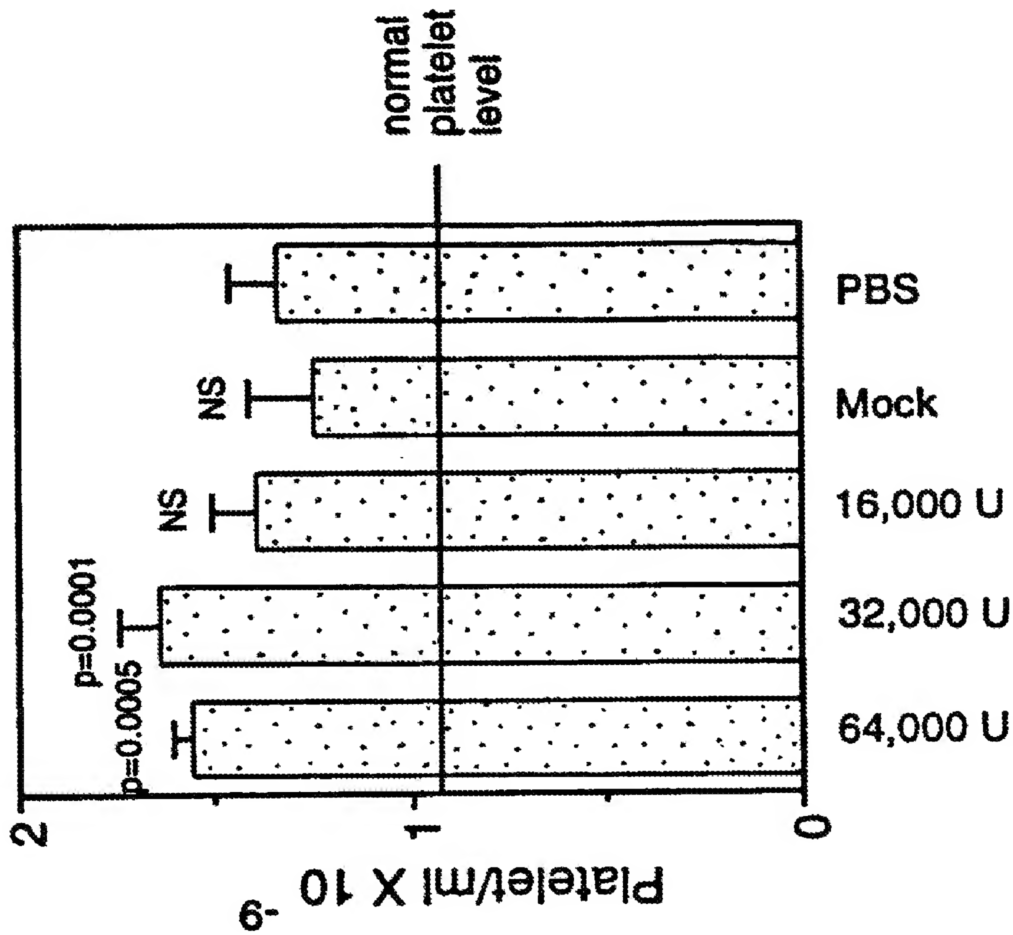


FIG. 12D



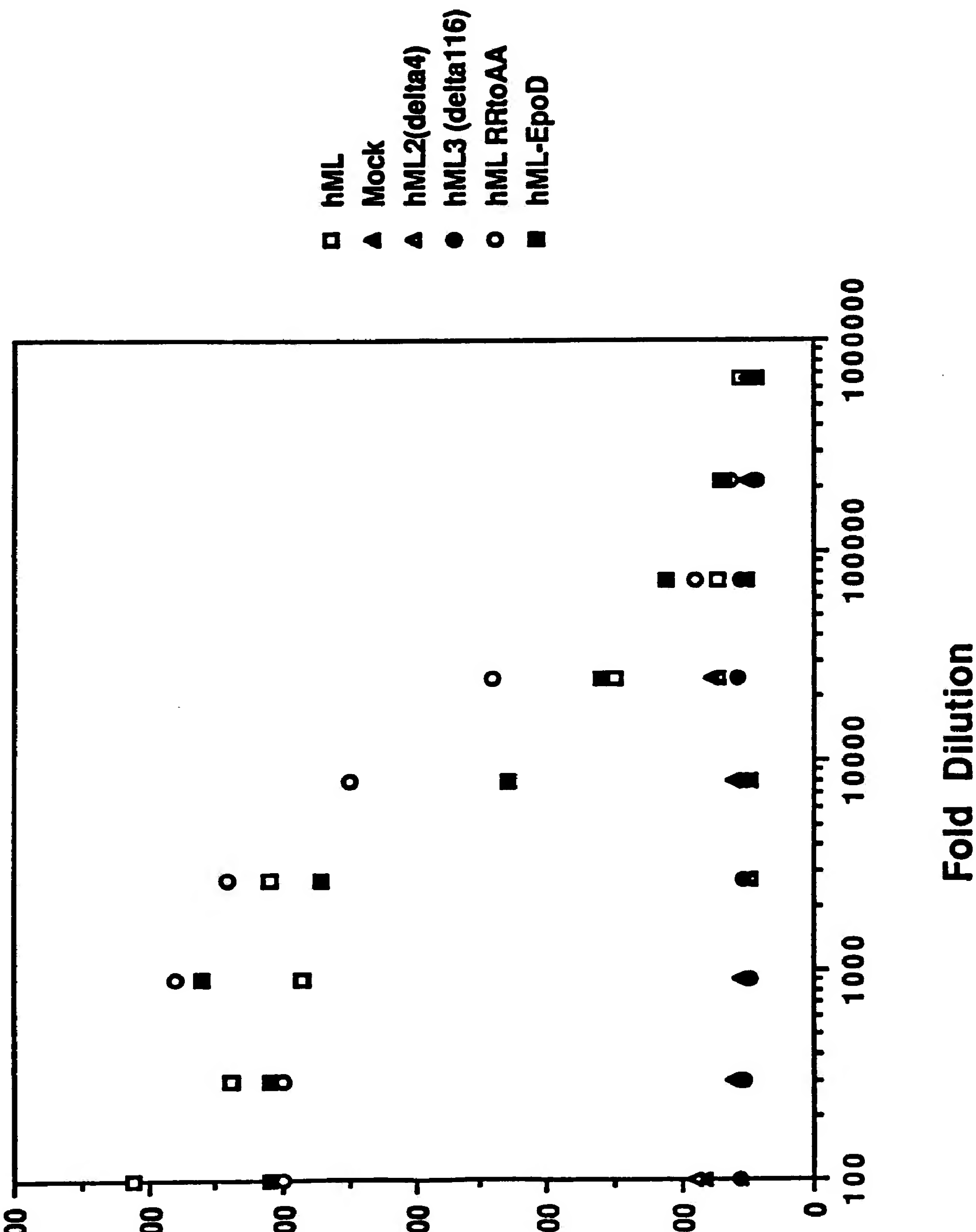

[3H]-Thymidine Incorporation
60000
50000
40000
30000
20000
10000
0
100
1000
10000
100000
1000000
Fold Dilution
hML
Mock
hML2(delta4)
hML3 (delta116)
hML RRtoAA
hML-EpoD

FIG. 13

FIG. 14

FIG.14A

```
   1 GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC

                                          -20                                      -10
                                      Met GluLeuThrA spLeuLeuLe uAlaAlaMet LeuLeuAlaV alAlaArgLe uThrLeuSer
 101 ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC

                                 10                     20                     30
     SerProValA laProAlaCy sAspProArg LeuLeuAsnL ysLeuLeuAr gAspSerHis LeuLeuHisS erArgLeuSe rGlnCysPro AspValAspPro
 201 AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC

                      40                    50                     60
     LeuSerIl eProValLeu LeuProAlaV alAspPheSe rLeuGlyGlu TrpLysThrG lnThrGluGl nSerLysAla GlnAspIleL euGlyAlaVal
 301 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT

          70                     80                     90                     100
     SerLeuLeu LeuGluGlyV alMetAlaAl aArgGlyGln LeuGluProS erCysLeuSe rSerLeuLeu GlyGlnLeuS erGlyGlnVa lArgLeuLeu
 401 GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC

                                110                    120                    130
     LeuGlyAlaL euGlnGlyLe uLeuGlyThr GlnGlyArgT hrThrAlaHi sLysAspPro AsnAlaLeuP heLeuSerLe uGlnGlnLeu LeuArgGlyLys
 501 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTCGGGGAA

                     140                    150                    160
     ValArgPh eLeuLeuLeu ValGluGlyP roThrLeuCy sValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
 601 AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT
```

FIG.14B

```
          170                    180                    190                    200
     AsnLysPhe ProAsnArgT hrSerGlyLe uLeuGluThr AsnPheSerV alThrAlaAr gThrAlaGly ProGlyLeuL euSerArgLe uGlnGlyPhe
 701 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC

                                210                    220                    230
     ArgValLysI leThrProGl yGlnLeuAsn GlnThrSerA rgSerProVa lGlnIleSer GlyTyrLeuA snArgThrHi sGlyProVal AsnGlyThrHis
 801 AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC

                     240                    250                    260
     GlyLeuPh eAlaGlyThr SerLeuGlnT hrLeuGluAl aSerAspIle SerProGlyA laPheAsnLy sGlySerLeu AlaPheAsnL euGlnGlyGly
 901 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG

          270                    280                    290                    300
     LeuProPro SerProSerL euAlaProAs pGlyHisThr ProPheProP roSerProAl aLeuProThr ThrHisGlyS erProProGl nLeuHisPro
1001 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC CTTCACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC

                                310                    320                    330
     LeuPheProA spProSerTh rThrMetPro AsnSerThrA laProHisPr oValThrMet TyrProHisP roArgAsnLe uSerGlnGlu Thr
1101 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG

1201 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT

1301 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA

1401 TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT TCT
```

FIG. 14A

```
  1 GAGTCCTTGG CCCACCTCTC TCCCACCCGA CTCTGCCGAA AGAAGCACAG AAGCTCAAGC CGCCTCCATG GCCCCAGGAA AGATTCAGGG GAGAGGCCCC

                                                 -20                              -10                     ↓
                                             Met GluLeuThrA spLeuLeuLe uAlaAlaMet LeuLeuAlaV alAlaArgLe uThrLeuSer
101 ATACAGGGAG CCACTTCAGT TAGACACCCT GGCCAGAATG GAGCTGACTG ATTTGCTCCT GGCGGCCATG CTTCTTGCAG TGGCAAGACT AACTCTGTCC

                          10                               20                               30
    SerProValA laProAlaCy sAspProArg LeuLeuAsnL ysLeuLeuAr gAspSerHis LeuLeuHisS erArgLeuSe rGlnCysPro AspValAspPro
201 AGCCCCGTAG CTCCTGCCTG TGACCCCAGA CTCCTAAATA AACTGCTGCG TGACTCCCAC CTCCTTCACA GCCGACTGAG TCAGTGTCCC GACGTCGACC

               40                               50                               60
    LeuSerIl eProValLeu LeuProAlaV alAspPheSe rLeuGlyGlu TrpLysThrG lnThrGluGl nSerLysAla GlnAspIleL euGlyAlaVal
301 CTTTGTCTAT CCCTGTTCTG CTGCCTGCTG TGGACTTTAG CCTGGGAGAA TGGAAAACCC AGACGGAACA GAGCAAGGCA CAGGACATTC TAGGGGCAGT

     70                              80                               90                                         100
    SerLeuLeu LeuGluGlyV alMetAlaAl aArgGlyGln LeuGluProS erCysLeuSe rSerLeuLeu GlyGlnLeuS erGlyGlnVa lArgLeuLeu
401 GTCCCTTCTA CTGGAGGGAG TGATGGCAGC ACGAGGACAG TTGGAACCCT CCTGCCTCTC ATCCCTCCTG GGACAGCTTT CTGGGCAGGT TCGCCTCCTC

                          110                              120                              130
    LeuGlyAlaL euGlnGlyLe uLeuGlyThr GlnGlyArgT hrThrAlaHi sLysAspPro AsnAlaLeuP heLeuSerLe uGlnGlnLeu LeuArgGlyLys
501 TTGGGGGCCC TGCAGGGCCT CCTAGGAACC CAGGGCAGGA CCACAGCTCA CAAGGACCCC AATGCCCTCT TCTTGAGCTT GCAACAACTG CTTCGGGGAA

               140                              150                              160
    ValArgPh eLeuLeuLeu ValGluGlyP roThrLeuCy sValArgArg ThrLeuProT hrThrAlaVa lProSerSer ThrSerGlnL euLeuThrLeu
601 AGGTGCGCTT CCTGCTTCTG GTAGAAGGTC CCACCCTCTG TGTCAGACGG ACCCTGCCAA CCACAGCTGT CCCAAGCAGT ACTTCTCAAC TCCTCACACT
```

FIG. 14B

```
                170                                180                                 190                                 200
     AsnLysPhe ProAsnArgT hrSerGlyLe uLeuGluThr AsnPheSerV alThrAlaAr gThrAlaGly ProGlyLeuL euSerArgLe uGlnGlyPhe
 701 AAACAAGTTC CCAAACAGGA CTTCTGGATT GTTGGAGACG AACTTCAGTG TCACAGCCAG AACTGCTGGC CCTGGACTTC TGAGCAGGCT TCAGGGATTC

                                      210                                 220                                 230
     ArgValLysI leThrProGl yGlnLeuAsn GlnThrSerA rgSerProVa lGlnIleSer GlyTyrLeuA snArgThrHi sGlyProVal AsnGlyThrHis
 801 AGAGTCAAGA TTACTCCTGG TCAGCTAAAT CAAACCTCCA GGTCCCCAGT CCAAATCTCT GGATACCTGA ACAGGACACA CGGACCTGTG AATGGAACTC

                           240                                 250                                 260
      GlyLeuPh eAlaGlyThr SerLeuGlnT hrLeuGluAl aSerAspIle SerProGlyA laPheAsnLy sGlySerLeu AlaPheAsnL euGlnGlyGly
 901 ATGGGCTCTT TGCTGGAACC TCACTTCAGA CCCTGGAAGC CTCAGACATC TCGCCCGGAG CTTTCAACAA AGGCTCCCTG GCATTCAACC TCCAGGGTGG

                270                                280                                 290                                 300
      LeuProPro SerProSerL euAlaProAs pGlyHisThr ProPheProP roSerProAl aLeuProThr ThrHisGlyS erProProGl nLeuHisPro
1001 ACTTCCTCCT TCTCCAAGCC TTGCTCCTGA TGGACACACA CCCTTCCCTC CTTCACCTGC CTTGCCCACC ACCCATGGAT CTCCACCCCA GCTCCACCCC

                                      310                                 320                                 330
     LeuPheProA spProSerTh rThrMetPro AsnSerThrA laProHisPr oValThrMet TyrProHisP roArgAsnLe uSerGlnGlu Thr
1101 CTGTTTCCTG ACCCTTCCAC CACCATGCCT AACTCTACCG CCCCTCATCC AGTCACAATG TACCCTCATC CCAGGAATTT GTCTCAGGAA ACATAGCGCG

1201 GGCACTGGCC CAGTGAGCGT CTGCAGCTTC TCTCGGGGAC AAGCTTCCCC AGGAAGGCTG AGAGGCAGCT GCATCTGCTC CAGATGTTCT GCTTTCACCT

1301 AAAAGGCCCT GGGGAAGGGA TACACAGCAC TGGAGATTGT AAAATTTTAG GAGCTATTTT TTTTTAACCT ATCAGCAATA TTCATCAGAG CAGCTAGCGA

1401 TCTTTGGTCT ATTTTCGGTA TAAATTTGAA AATCACTAAT TCT
```

FIG. 15

FIG.15A

```
   1 gagtccttggcccacctctctcccacccgactctgccgaaagaagcacagaagctcaagccgcctccatggccccaggaaagattcaggggagaggcccc

                                         -20                           -10                  ↓
                                         MetGluLeuThrAspLeuLeuLeuAlaAlaMetLeuLeuAlaValAlaArgLeuThrLeuSer
 101 atacagggagccacttcagttagacaccctggccagaATGGAGCTGACTGATTTGCTCCTGGCGGCCATGCTTCTTGCAGTGGCAAGACTAACTCTGTCC

                          •    10                            20                            • 30
     SerProValAlaProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisLeuLeuHisSerArgLeuSerGlnCysProAspValAspPro
 201 AGCCCCGTAGCTCCTGCCTGTGACCCCAGACTCCTAAATAAACTGCTGCGTGACTCCCACCTCCTTCACAGCCGACTGAGTCAGTGTCCCGACGTCGACC

                          40                            50                            60
      LeuSerIleProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnThrGluGlnSerLysAlaGlnAspIleLeuGlyAlaVal
 301 CTTTGTCTATCCCTGTTCTGCTGCCTGCTGTGGACTTTAGCCTGGGAGAATGGAAAACCCAGACGGAACAGAGCAAGGCACAGGACATTCTAGGGGCAGT

           70                            80         •                 90                            100
      SerLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGluProSerCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
 401 GTCCCTTCTACTGGAGGGAGTGATGGCAGCACGAGGACAGTTGGAACCCTCCTGCCTCTCATCCCTCCTGGGACAGCTTTCTGGGCAGGTTCGCCTCCTC

                               110                            120                            130
     LeuGlyAlaLeuGlnGlyLeuLeuGlyThrGlnLeuProLeuGlnGlyArgThrThrAlaHisLysAspProAsnAlaLeuPheLeuSerLeuGlnGlnLeu
 501 TTGGGGGCCCTGCAGGGCCTCCTAGGAACCCAGCTTCCTCTACAGGGCAGGACCACAGCTCACAAGGACCCCAATGCCCTCTTCTTGAGCTTGCAACAAC

                          140                           150 •                          160
      LeuArgGlyLysValArgPheLeuLeuLeuValGluGlyProThrLeuCysValArgArgThrLeuProThrThrAlaValProSerSerThrSerGln
 601 TGCTTCGGGGAAAGGTGCGCTTCCTGCTTCTGGTAGAAGGTCCCACCCTCTGTGTCAGACGGACCCTGCCAACCACAGCTGTCCCAAGCAGTACTTCTCA

           170                           180                           190                           200
      LeuLeuThrLeuAsnLysPheProAsnArgThrSerGlyLeuLeuGluThrAsnPheSerValThrAlaArgThrAlaGlyProGlyLeuLeuSerArg
 701 ACTCCTCACACTAAACAAGTTCCCAAACAGGACTTCTGGATTGTTGGAGACGAACTTCAGTGTCACAGCCAGAACTGCTGGCCCTGGACTTCTGAGCAGG
```

FIG.15B

```
                               210                           220                           230
     LeuGlnGlyPheArgValLysIleThrProGlyGlnLeuAsnGlnThrSerArgSerProValGlnIleSerGlyTyrLeuAsnArgThrHisGlyProVal
 801 CTTCAGGGATTCAGAGTCAAGATTACTCCTGGTCAGCTAAATCAAACCTCCAGGTCCCCAGTCCAAATCTCTGGATACCTGAACAGGACACACGGACCTG

                          240                           250                           260
      AsnGlyThrHisGlyLeuPheAlaGlyThrSerLeuGlnThrLeuGluAlaSerAspIleSerProGlyAlaPheAsnLysGlySerLeuAlaPheAsn
 901 TGAATGGAACTCATGGGCTCTTTGCTGGAACCTCACTTCAGACCCTGGAAGCCTCAGACATCTCGCCCGGAGCTTTCAACAAAGGCTCCCTGGCATTCAA

           270                           280                           290                           300
      LeuGlnGlyGlyLeuProProSerProSerLeuAlaProAspGlyHisThrProPheProProSerProAlaLeuProThrThrHisGlySerProPro
1001 CCTCCAGGGTGGACTTCCTCCTTCTCCAAGCCTTGCTCCTGATGGACACACACCCTTCCCTCCTTCACCTGCCTTGCCCACCACCCATGGATCTCCACCC

                               310                           320                           330
     GlnLeuHisProLeuPheProAspProSerThrThrMetProAsnSerThrAlaProHisProValThrMetTyrProHisProArgAsnLeuSerGlnGlu
1101 CAGCTCCACCCCCTGTTTCCTGACCCTTCCACCACCATGCCTAACTCTACCGCCCCTCATCCAGTCACAATGTACCCTCATCCCAGGAATTTGTCTCAGG

      Thr
1201 AAACATAGcgcgggcactggcccagtgagcgtctgcagcttctctcggggacaagcttccccaggaaggctgagaggcagctgcatctgctccagatgtt

1301 ctgctttcacctaaaaggccctggggaagggatacacagcactggagattgtaaaatttaggagctatttttttttaacctatcagcaatattcatcag

1401 agcagctagcgatctttggtctattttcggtataaatttgaaaatcactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

1501 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

FIG. 15A

```
  1 gagtccttggcccacctctctcccacccgactctgccgaaagaagcacagaagctcaagccgcctccatggccccaggaaagattcaggggagaggcccc

                                                        -20                                -10
                                                     MetGluLeuThrAspLeuLeuLeuAlaAlaMetLeuLeuAlaValAlaArgLeuThrLeuSer
101 atacagggagccacttcagttagacaccctggccagaATGGAGCTGACTGATTTGCTCCTGGCGGCCATGCTTCTTGCAGTGGCAAGACTAACTCTGTCC

                                 10                                20                               30
    SerProValAlaProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisLeuLeuHisSerArgLeuSerGlnCysProAspValAspPro
201 AGCCCCGTAGCTCCTGCCTGTGACCCCAGACTCCTAAATAAACTGCTGCGTGACTCCCACCTCCTTCACAGCCGACTGAGTCAGTGTCCCGACGTCGACC

                      40                                50                                60
      LeuSerIleProValLeuLeuProAlaValAspPheSerLeuGlyGluTrpLysThrGlnThrGluGlnSerLysAlaGlnAspIleLeuGlyAlaVal
301 CTTTGTCTATCCCTGTTCTGCTGCCTGCTGTGGACTTTAGCCTGGGAGAATGGAAAACCCAGACGGAACAGAGCAAGGCACAGGACATTCTAGGGGCAGT

            70                                80                                90                                100
     SerLeuLeuLeuGluGlyValMetAlaAlaArgGlyGlnLeuGluProSerCysLeuSerSerLeuLeuGlyGlnLeuSerGlyGlnValArgLeuLeu
401 GTCCCTTCTACTGGAGGGAGTGATGGCAGCACGAGGACAGTTGGAACCCTCCTGCCTCTCATCCCTCCTGGGACAGCTTTCTGGGCAGGTTCGCCTCCTC

                                 110                               120                               130
    LeuGlyAlaLeuGlnGlyLeuLeuGlyThrGlnLeuProLeuGlnGlyArgThrThrAlaHisLysAspProAsnAlaLeuPheLeuSerLeuGlnGlnLeu
501 TTGGGGGCCCTGCAGGGCCTCCTAGGAACCCAGCTTCCTCTACAGGGCAGGACCACAGCTCACAAGGACCCCAATGCCCTCTTCTTGAGCTTGCAACAAC

                      140                               150                               160
      LeuArgGlyLysValArgPheLeuLeuLeuValGluGlyProThrLeuCysValArgArgThrLeuProThrThrAlaValProSerSerThrSerGln
601 TGCTTCGGGGAAAGGTGCGCTTCCTGCTTCTGGTAGAAGGTCCCACCCTCTGTGTCAGACGGACCCTGCCAACCACAGCTGTCCCAAGCAGTACTTCTCA

            170                               180                               190                               200
     LeuLeuThrLeuAsnLysPheProAsnArgThrSerGlyLeuLeuGluThrAsnPheSerValThrAlaArgThrAlaGlyProGlyLeuLeuSerArg
701 ACTCCTCACACTAAACAAGTTCCCAAACAGGACTTCTGGATTGTTGGAGACGAACTTCAGTGTCACAGCCAGAACTGCTGGCCCTGGACTTCTGAGCAGG
```

FIG. 15B

```
                                210                                 220                                 230
     LeuGlnGlyPheArgValLysIleThrProGlyGlnLeuAsnGlnThrSerArgSerProValGlnIleSerGlyTyrLeuAsnArgThrHisGlyProVal
 801 CTTCAGGGATTCAGAGTCAAGATTACTCCTGGTCAGCTAAATCAAACCTCCAGGTCCCCAGTCCAAATCTCTGGATACCTGAACAGGACACACGGACCTG

                      240                                 250                                 260
       AsnGlyThrHisGlyLeuPheAlaGlyThrSerLeuGlnThrLeuGluAlaSerAspIleSerProGlyAlaPheAsnLysGlySerLeuAlaPheAsn
 901 TGAATGGAACTCATGGGCTCTTTGCTGGAACCTCACTTCAGACCCTGGAAGCCTCAGACATCTCGCCCGGAGCTTTCAACAAAGGCTCCCTGGCATTCAA

        270                                 280                                 290                                 300
      LeuGlnGlyGlyLeuProProSerProSerLeuAlaProAspGlyHisThrProPheProProSerProAlaLeuProThrThrHisGlySerProPro
1001 CCTCCAGGGTGGACTTCCTCCTTCTCCAAGCCTTGCTCCTGATGGACACACACCCTTCCCTCCTTCACCTGCCTTGCCCACCACCCATGGATCTCCACCC

                                310                                 320                                 330
     GlnLeuHisProLeuPheProAspProSerThrThrMetProAsnSerThrAlaProHisProValThrMetTyrProHisProArgAsnLeuSerGlnGlu
1101 CAGCTCCACCCCCTGTTTCCTGACCCTTCCACCACCATGCCTAACTCTACCGCCCCTCATCCAGTCACAATGTACCCTCATCCCAGGAATTTGTCTCAGG

       Thr
1201 AAACATAGcgcgggcactggcccagtgagcgtctgcagcttctctcggggacaagcttccccaggaaggctgagaggcagctgcatctgctccagatgtt

1301 ctgctttcacctaaaaggcccctggggaagggatacacagcactggagattgtaaaattttaggagctattttttttaacctatcagcaatattcatcag

1401 agcagctagcgatctttggtctattttcggtataaatttgaaaatcactaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa

1501 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
```

FIG. 16

```
hML3    1   SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE
mML3    1   SPVAPACDPRLLNKLLRDSHLLHSRLSQCPDVDPLSIPVLLPAVDFSLGE

hML3   51   WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL
mML3   51   WKTQTEQSKAQDILGAVSLLLEGVMAARGQLEPSCLSSLLGQLSGQVRLL

hML3  101   LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKDFWIVGDKLHCL
mML3  101   LGALQGLLGTQLPLQGRTTAHKDPNALFLSLQOLLRGKDFWIVGDELQCH

hML3  151   SQNYWLWASEVAAGIQSQD.SWSAEPNLQVPGPNPRIPEQDTRTLEWNSW
mML3  151   SQNCWPWTSEQASGIQSQDYSWSAKSNLQVPSPNLWIPEQDTRTCEWNSW

hML3  200   TLSWTLTQDPRSPGHFLRNIRHRLPATQPPAWIFSFPNPSSYWTVYALPS
mML3  201   ALCWNLTSDPGSLRHLARSFQORLPGIQPPGWTSSFSKPCS

hML3  250   STHLAHPCGPAPPPAS
```

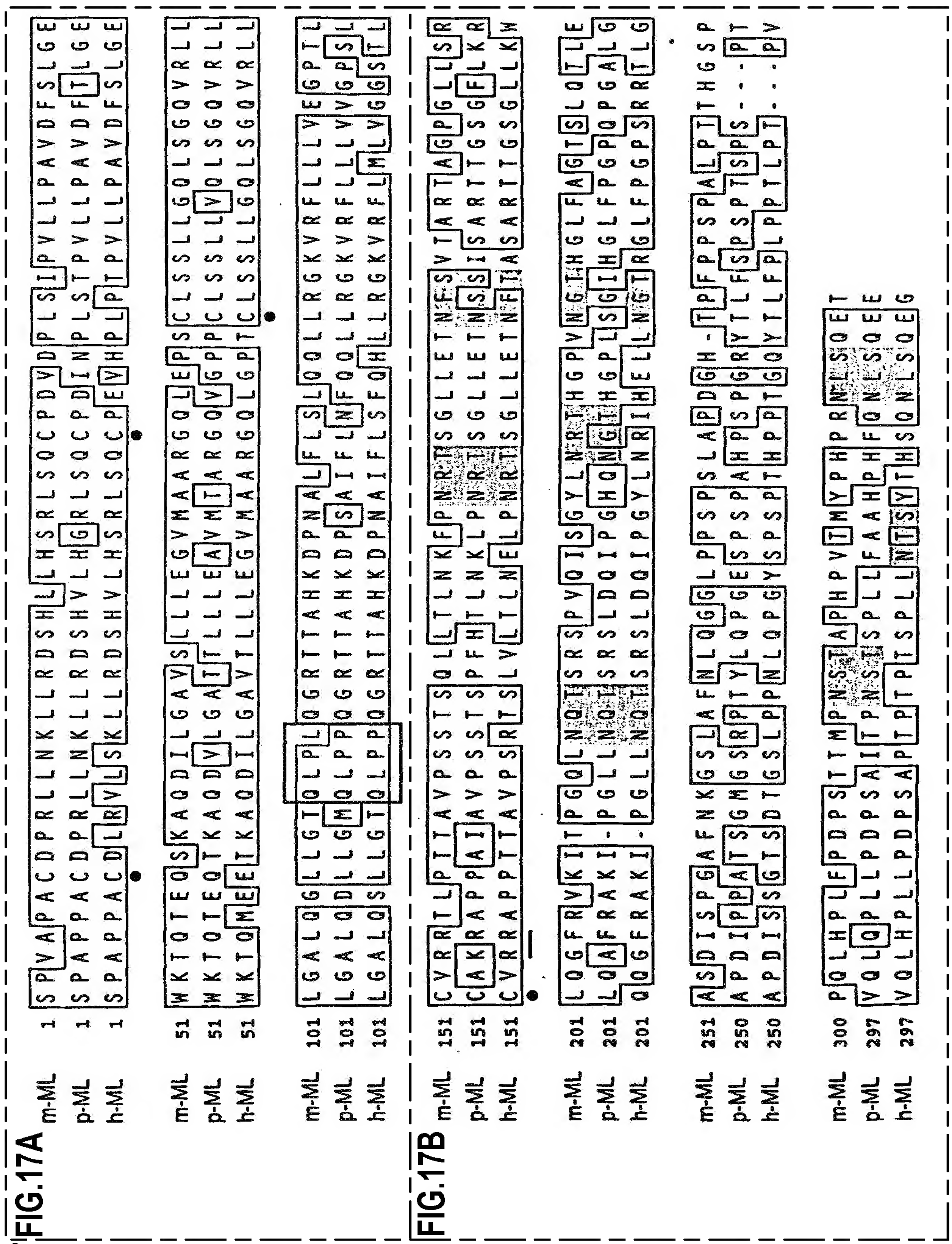


FIG. 17

FIG. 17A

```
m-ML   1 SPVAPACDPRLLNKLLRDSHLLHSRLSQCPDVDPLSIPVLLPAVDFSLGE
p-ML   1 SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
h-ML   1 SPAPPACDLRVLSKLLRDSHVLHSRLSQCPEVHPLPTPVLLPAVDFSLGE

m-ML  51 WKTQTEQSKAQDILGAVSLLLEGVMAARGQLEPSCLSSLLGQLSGQVRLL
p-ML  51 WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
h-ML  51 WKTQMEETKAQDILGAVTLLLEGVMAARGQLGPTCLSSLLGQLSGQVRLL

m-ML 101 LGALQGLLGTQLPLQGRTTAHKDPNALFLSLQQLLRGKVRFLLLVEGPTL
p-ML 101 LGALQDLLGMQLPPQGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
h-ML 101 LGALQSLLGTQLPPQGRTTAHKDPNAIFLSFQHLLRGKVRFLMLVGGSTL
```

FIG.17B

```
m-ML  151  CVRRTLPTTAVPSSTSQLLTLNKFPNRTSGLLETNFSVTARTAGPGLLSR
p-ML  151  CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
h-ML  151  CVRRAPPTTAVPSRTSLVLTLNELPNRTSGLLETNFTASARTTGSGLLKW

m-ML  201  LQGFRVKITPGQLNQTSRSPVQISGYLNRTHGPVNGTHGLFAGTSLQTLE
p-ML  201  LQAFRAKI-PGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALG
h-ML  201  QQGFRAKI-PGLLNQTSRSLDQIPGYLNRIHELLNGTRGLFPGPSRRTLG

m-ML  251  ASDISPGAFNKGSLAFNLQGGLPPSPSLAPDGH-TPFPPSPALPTTHGSP
p-ML  250  APDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPS---PT
h-ML  250  APDISSGTSDTGSLPPNLQPGYSPSPTHPPTGQYTLFPLPPTLPT---PV

m-ML  300  PQLHPLFPDPSTTMPNSTAPHPVTMYPHPRNLSQET
p-ML  297  VQLQPLLPDPSAITPNSTSPLLFAAHPHFQNLSQEE
h-ML  297  VQLHPLLPDPSAPTPTPTSPLLNTSYTHSQNLSQEG
```

FIG. 18

FIG.18A

```
                             10                            20                            30
     SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
   1 AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC

                   40                            50                            60
      LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
 101 CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC

         70                            80                            90                            100
      ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
 201 AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC

                             110                           120                           130
     LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeu
 301 CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGCTTCCTCCACAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAAC

                   140                           150                           160
      LeuArgGlyLysValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerPro
 401 TGCTCCGAGGAAAGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCC

         170                           180                           190                           200
      PheHisThrLeuAsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArg
 501 ATTCCACACACTGAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGG
```

FIG.18B

```
                             210                           220                           230
     LeuGlnAlaPheArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSer
 601 CTGCAGGCATTCAGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGA

                   240                           250                           260
      GlyIleHisGlyLeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeu
 701 GTGGAATTCATGGACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCT

         270                           280                           290                           300
      GlnProGlyGluSerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGln
 801 CCAGCCTGGAGAGTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAG

                             310                           320                           330
     ProLeuLeuProAspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
 901 CCTCTGCTTCCTGACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAG

1001 GTGCTCAGACCCTGCCAACTTCAGCA
```

FIG.18A

```
                                   10                                  20                                  30
    SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
  1 AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC

                        40                                  50                                  60
      LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
101 CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC

             70                                  80                                  90                                 100
     ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
201 AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC

                                  110                                 120                                 130
    LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnLeuProProGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeu
301 CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGCTTCCTCCACAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAAC

                        140                                 150                                 160
      LeuArgGlyLysValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerPro
401 TGCTCCGAGGAAAGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCC

             170                                 180                                 190                                 200
     PheHisThrLeuAsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArg
501 ATTCCACACACTGAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGG
```

FIG. 18B

```
                                   210                                   220                                   230
      LeuGlnAlaPheArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSer
 601 CTGCAGGCATTCAGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGA

                        240                                   250                                   260
       GlyIleHisGlyLeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeu
 701 GTGGAATTCATGGACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGCTCCCGGCCAACCTACCT

            270                                   280                                   290                                   300
      GlnProGlyGluSerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGln
 801 CCAGCCTGGAGAGTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAG

                                   310                                   320                                   330
      ProLeuLeuProAspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
 901 CCTCTGCTTCCTGACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAG

1001 GTGCTCAGACCCTGCCAACTTCAGCA
```

FIG. 19

FIG. 19A

```
                              10                                      20                                      30
        SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
      1 AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC

                    40                                      50                                      60
          LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
    101 CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC

           70                                      80                                      90                                     100
         ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
    201 AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC

                              110                                     120                                     130
        LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeuLeuArgGlyLys
    301 CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAACTGCTCCGAGGAA

                    140                                     150                                     160
          ValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerProPheHisThrLeu
    401 AGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCCATTCCACACACT
```

FIG.19B

```
           170                                     180                                     190                                     200
         AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe
    501 GAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGGCTGCAGGCATTC

                              210                                     220                                     230
        ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly
    601 AGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGAGTGGAATTCATG

                    240                                     250                                     260
          LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeuGlnProGlyGlu
    701 GACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCTCCAGCCTGGAGA

           270                                     280                                     290                                     300
         SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro
    801 GTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAGCCTCTGCTTCCT

                              310                                     320
        AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
    901 GACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAGGTGCTCAGACCC

   1001 TGCCAACTTCAGCA
```

FIG. 19A

```
                                        10                                      20                                      30
      SerProAlaProProAlaCysAspProArgLeuLeuAsnLysLeuLeuArgAspSerHisValLeuHisGlyArgLeuSerGlnCysProAspIleAsnPro
  1   AGCCCGGCTCCTCCTGCCTGTGACCCCCGACTCCTAAATAAACTGCTTCGTGACTCCCATGTCCTTCACGGCAGACTGAGCCAGTGCCCAGACATTAACC

                           40                                      50                                      60
       LeuSerThrProValLeuLeuProAlaValAspPheThrLeuGlyGluTrpLysThrGlnThrGluGlnThrLysAlaGlnAspValLeuGlyAlaThr
101   CTTTGTCCACACCTGTCCTGCTGCCTGCTGTGGACTTCACCTTGGGAGAATGGAAAACCCAGACGGAGCAGACAAAGGCACAGGATGTCCTGGGAGCCAC

               70                                      80                                      90                                     100
      ThrLeuLeuLeuGluAlaValMetThrAlaArgGlyGlnValGlyProProCysLeuSerSerLeuLeuValGlnLeuSerGlyGlnValArgLeuLeu
201   AACCCTTCTGCTGGAGGCAGTGATGACAGCACGGGGACAAGTGGACCCCCTTGCCTCTCATCCCTGCTGGTGCAGCTTTCTGGACAGGTTCGCCTCCTC

                                        110                                     120                                     130
      LeuGlyAlaLeuGlnAspLeuLeuGlyMetGlnGlyArgThrThrAlaHisLysAspProSerAlaIlePheLeuAsnPheGlnGlnLeuLeuArgGlyLys
301   CTCGGGGCCCTGCAGGACCTCCTTGGAATGCAGGGAAGGACCACAGCTCACAAGGATCCCAGTGCCATCTTCCTGAACTTCCAACAACTGCTCCGAGGAA

                           140                                     150                                     160
       ValArgPheLeuLeuLeuValValGlyProSerLeuCysAlaLysArgAlaProProAlaIleAlaValProSerSerThrSerProPheHisThrLeu
401   AGGTGCGTTTCCTGCTCCTTGTAGTGGGGCCCTCCCTCTGTGCCAAGAGGGCCCCACCCGCCATAGCTGTCCCGAGCAGCACCTCTCCATTCCACACACT
```

FIG. 19B

```
                170                    180                    190                    200
     AsnLysLeuProAsnArgThrSerGlyLeuLeuGluThrAsnSerSerIleSerAlaArgThrThrGlySerGlyPheLeuLysArgLeuGlnAlaPhe
 501 GAACAAGCTCCCAAACAGGACCTCTGGATTGTTGGAGACAAACTCCAGTATCTCAGCCAGAACTACTGGCTCTGGATTTCTCAAGAGGCTGCAGGCATTC

                            210                    220                    230
     ArgAlaLysIleProGlyLeuLeuAsnGlnThrSerArgSerLeuAspGlnIleProGlyHisGlnAsnGlyThrHisGlyProLeuSerGlyIleHisGly
 601 AGAGCCAAGATTCCTGGTCTGCTGAACCAAACCTCCAGGTCCCTAGACCAAATCCCTGGACACCAGAATGGGACACACGGACCCTTGAGTGGAATTCATG

                      240                    250                    260
      LeuPheProGlyProGlnProGlyAlaLeuGlyAlaProAspIleProProAlaThrSerGlyMetGlySerArgProThrTyrLeuGlnProGlyGlu
 701 GACTCTTTCCTGGACCCCAACCCGGGGCCCTCGGAGCTCCAGACATTCCTCCAGCAACTTCAGGCATGGGCTCCCGGCCAACCTACCTCCAGCCTGGAGA

                270                    280                    290                    300
     SerProSerProAlaHisProSerProGlyArgTyrThrLeuPheSerProSerProThrSerProSerProThrValGlnLeuGlnProLeuLeuPro
 801 GTCTCCTTCCCCAGCTCACCCTTCTCCTGGACGATACACTCTCTTCTCTCCTTCACCCACCTCGCCCTCCCCCACAGTCCAGCTCCAGCCTCTGCTTCCT

                            310                    320
     AspProSerAlaIleThrProAsnSerThrSerProLeuLeuPheAlaAlaHisProHisPheGlnAsnLeuSerGlnGluGlu
 901 GACCCCTCTGCGATCACACCCAACTCTACCAGTCCTCTTCTATTTGCAGCTCACCCTCATTTCCAGAACCTGTCTCAGGAAGAGTAAGGTGCTCAGACCC

1001 TGCCAACTTCAGCA
```

FIG. 20

FIG.20A

pML	1	SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML2	1	SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML	51	WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML2	51	WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML	101	LGALQDLLGMQLPPQGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
pML2	101	LGALQDLLGM....QGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL

FIG.20B

pML	151	CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
pML2	147	CAKRAPPAIAVPSSTSPFHTLNKLPNRTSGLLETNSSISARTTGSGFLKR
pML	201	LQAFRAKIPGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALGA
pML2	197	LQAFRAKIPGLLNQTSRSLDQIPGHQNGTHGPLSGIHGLFPGPQPGALGA
pML	251	PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ
pML2	247	PDIPPATSGMGSRPTYLQPGESPSPAHPSPGRYTLFSPSPTSPSPTVQLQ
pML	301	PLLPDPSAITPNSTSPLLFAAHPHFQNLSQEE
pML2	297	PLLPDPSAITPNSTSPLLFAAHPHFQNLSQEE

FIG. 20A

```
pML    1   SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE
pML2   1   SPAPPACDPRLLNKLLRDSHVLHGRLSQCPDINPLSTPVLLPAVDFTLGE

pML    51  WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL
pML2   51  WKTQTEQTKAQDVLGATTLLLEAVMTARGQVGPPCLSSLLVQLSGQVRLL

pML    101 LGALQDLLGMQLPPQGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
pML2   101 LGALQDLLGM....QGRTTAHKDPSAIFLNFQQLLRGKVRFLLLVVGPSL
```

FIG. 20B

pML	151	C A K R A P P A I A V P S S T S P F H T L N K L P N R T S G L L E T N S S I S A R T T G S G F L K R
pML2	147	C A K R A P P A I A V P S S T S P F H T L N K L P N R T S G L L E T N S S I S A R T T G S G F L K R
pML	201	L Q A F R A K I P G L L N Q T S R S L D Q I P G H Q N G T H G P L S G I H G L F P G P Q P G A L G A
pML2	197	L Q A F R A K I P G L L N Q T S R S L D Q I P G H Q N G T H G P L S G I H G L F P G P Q P G A L G A
pML	251	P D I P P A T S G M G S R P T Y L Q P G E S P S P A H P S P G R Y T L F S P S P T S P S P T V Q L Q
pML2	247	P D I P P A T S G M G S R P T Y L Q P G E S P S P A H P S P G R Y T L F S P S P T S P S P T V Q L Q
pML	301	P L L P D P S A I T P N S T S P L L F A A H P H F Q N L S Q E E
pML2	297	P L L P D P S A I T P N S T S P L L F A A H P H F Q N L S Q E E